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Identification And Characterisation Of A Novel MicroRNA Implicated In Phosphate Homeostasis In Rice

Carole Santi¹, Elodie Lacut², Emmanuel Guiderdoni², Jean Luc Verdeil², Tzyy Jen Chiou³, Manuel Echeverria¹

- ¹ Génome et Développement des Plantes UMR 5096 Université de Perpignan-CNRS-IRD
52, Av. Paul Alduy, 66860 Perpignan Cedex, France
- ² Plant Development and genetic improvement UMR DAP 1098, CIRAD F 34398 Montpellier
Cedex 5, France.
- ³ Agricultural Biotechnology Research Center, Academia Sinica, Taipei 115, Taiwan

MicroRNAs represent a major class of small RNAs with master regulatory functions in plants. They are 20 to 22 nt single stranded RNAs encoded by endogenous genes. These are transcribed by RNA pol II. This produces a precursor-miRNA with a stem loop structure, subsequently processed by DCL activities to liberate the miRNA. The mature miRNA is incorporated into a RISC complex that direct cleavage of a specific target mRNA. Most mRNA targets encode transcription factors or signalling proteins that control diverse stages of development in plants. In our laboratory we are interested in the identification and characterisation of novel miRNAs which control development and growth in rice. To this aim we prepared individual cDNA libraries derived from a small RNA fraction extracted from leaves, seedlings, panicles and root, and identified many novel miRNAs. Here we focus on the functional characterisation of one of them, osa-miRD, which is implicated in phosphate homeostasis in rice. We demonstrate that osa-miRD target cleavage an mRNA encoding an SPX-domain containing protein, predicted to be implicated in phosphate or nutrient transport. Profiling of miRNA expression demonstrate that it is induced by Pi deprivation in both leaves and roots. In situ hybridisation confirms that osa-miRD is localised in vascular tissues. To confirm the implication of osa-miRD in phosphate homeostasis we have now produced rice transgenic lines overexpressing

osa-miRD. Phenotypic characterisation of these lines is being done to evaluate the effect on phosphate flux and the effect upon Pi deprivation of in these transgenic plants.

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